OM protein - protein search, using sw model

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GenCore version 4.5

Run on: February 13, 2001, 19:46:08 ; Search time 59.97 Seconds
                 (without alignments)
                 656.693 Million cell updates/sec

Title: US-09-481-990-2
Perfect score: 1753
Sequence: 1 MLQSLAGSSCVRLVERHRSA...........QNPFVATQSSACVDGPANH 336

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

earched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_15:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	1753	100.0	336	4	O00180	O00180 homo sapien
2	1693	96.6	336	11	Q92T2	Q92T2 rattus norv
3	1658	94.6	336	11	O08581	O08581 mus musculu
4	1292.5	73.7	259	6	O02821	O02821 oryctolagus
5	653.5	37.3	313	4	Q9Y257	Q9Y257 homo sapien
6	532.5	30.4	343	11	Q9JI14	Q9JI14 mus musculu
7	521.5	29.7	307	4	Q9Y2U2	Q9Y2U2 homo sapien
8	518.5	29.6	307	11	Q92T1	Q92T1 mus musculu
9	430.5	24.6	392	5	Q9NEV3	Q9NEV3 caenorhabdi
10	396	22.6	538	11	Q9IS4	Q9IS4 rattus norv
11	381.5	21.8	426	4	O95069	O95069 homo sapien
12	379.5	21.6	398	11	O08454	O08454 mus musculu
13	379.5	21.6	411	4	Q9NRT2	Q9NRT2 homo sapien
14	378	21.6	419	4	Q9NYG8	Q9NYG8 homo sapien
15	376.5	21.5	411	11	P97438	P97438 mus musculu
16	369	21.0	502	11	Q9JK62	Q9JK62 mus musculu
17	359	20.5	499	4	O95279	O95279 homo sapien
18	333.5	19.0	299	11	Q9QX34	Q9QX34 mus musculu
19	333.5	19.0	409	11	O35111	O35111 mus musculu

20	333.5	19.0	411	11	O54912	O54912 rattus norv
21	321.5	18.3	395	11	Q9JLD4	Q9JLD4 rattus norv
22	320.5	18.3	394	4	O14649	O14649 homo sapien
23	316.5	18.1	374	4	Q9NPC2	Q9NPC2 homo sapien
24	310	17.7	365	11	Q9JL58	Q9JL58 cavia porce
25	303.5	17.3	385	5	Q9VYY5	Q9VYY5 drosophila
26	300	17.1	393	5	Q9XU07	Q9XU07 drosophila
27	295	16.8	427	5	Q23386	Q23386 caenorhabdi
28	294.5	16.8	443	5	O45422	O45422 caenorhabdi
29	294	16.8	364	5	O76790	O76790 drosophila
30	291	16.6	329	5	O76795	O76795 caenorhabdi
31	284.5	16.2	995	5	O17185	O17185 caenorhabdi
32	278.5	15.9	340	5	O94526	O94526 drosophila
33	264.5	15.1	1001	5	Q9W2L7	Q9W2L7 drosophila
34	263	15.0	995	5	Q9W217	Q9W217 drosophila
35	256.5	14.6	475	5	Q23435	Q23435 caenorhabdi
36	251	14.3	383	5	Q21094	Q21094 caenorhabdi
37	251	14.3	398	5	Q9VFS9	Q9VFS9 drosophila
38	246	14.0	522	5	Q22042	Q22042 caenorhabdi
39	246	14.0	1910	5	Q22426	Q22426 caenorhabdi
40	245	14.0	395	5	Q9V362	Q9V362 drosophila
41	245	14.0	631	5	O45894	O45894 caenorhabdi
42	244	13.9	513	5	Q22940	Q22940 caenorhabdi
43	240	13.7	539	5	Q21505	Q21505 caenorhabdi
44	236	13.5	654	5	P90863	P90863 caenorhabdi
45	231	13.2	523	5	O17935	O17935 caenorhabdi

ALIGNMENTS

RESULT   1

O00180

O00180   PRELIMINARY;   PRT;   336 AA.

ID   O00180; Q13307;
AC   O00180;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1 (POTASSIUM CHANNEL
DE   KCNO1).
GN   KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC   TISSUE=KIDNEY;
RX   MEDLINE=96183184; PubMed=8605869;
RA   Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA   Barhanin J.;
RT   "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT   novel structure.";
RL   EMBO J. 15:1004-1011(1996).
RN   [2]
RP   SEQUENCE FROM N.A. AND REVIEW.
RC   TISSUE=BRAIN;
RX   MEDLINE=98122696; PubMed=9462864;
RA   Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
RT   "Sequence and function of the two P domain potassium channels:
RT   implications of an emerging superfamily.";
RL   J. Mol. Med. 76:13-20(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Desir G.V., Orias M., Freeman T.;
RL   Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC   BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC   -!- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
CC   INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

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CC    -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC        CHANNELS.
DR   EMBL; U33632; AAB01688.1; -.
DR   EMBL; U76996; AAB97878.1; -.
DR   EMBL; U90065; AAB51147.1; -.
DR   MIM; 601745; -.
DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   INTERPRO; IPR001779; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01333; 2POREKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     41       POTENTIAL.
FT   DOMAIN
FT   TRANSMEM    104    130       POTENTIAL.
FT   DOMAIN      133    153       POTENTIAL.
FT   TRANSMEM    154    177       POTENTIAL.
FT   TRANSMEM    178    198       POTENTIAL.
FT   DOMAIN      212    238       PORE-FORMING (POTENTIAL).
FT   TRANSMEM    247    267       POTENTIAL.
FT   DOMAIN      268    336       CYTOPLASMIC (POTENTIAL).
FT   POTENTIAL.
FT   POTENTIAL.
FT   PORE-FORMING (POTENTIAL).
FT   CYTOPLASMIC (POTENTIAL).
FT   POTENTIAL.
FT   POTENTIAL.
FT   MOD_RES      19     19       PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES     303    303       PHOSPHORYLATION (POTENTIAL).
FT   MOD_RES      95     95       PHOSPHORYLATION (BY CAM-KINASE II)
FT                                (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN     161    161       T->A: NO EFFECT ON CHANNEL ACTIVITY.
SQ   SEQUENCE   336 AA;  38143 MW;  2A41D95013232150 CRC64;

Query Match     100.0%;  Score 1753;  DB 4;  Length 336;
Best Local Similarity   100.0%;  Pred. No. 3.8e-135;
Matches  336;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLILYLVFGAVVFSSVELPYEDLLRQELRKLK  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLILYLVFGAVVFSSVELPYEDLLRQELRKLK  60

Qy   61  RRFLEEHECLSEQOLEQOFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  RRFLEEHECLSEQOLEQOFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120

Qy  121  GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180

Qy  181  IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240

Qy  241  FRELYKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQLS  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  FRELYKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQLS  300

Qy  301  FSSITDQAAGMKEDQKQNEPFVATQSSSACVDGPANH  336
         |||||||||||||||||||||||||||||||||||||
Db  301  FSSITDQAAGMKEDQKQNEPFVATQSSSACVDGPANH  336

RESULT  2
ID   Q92272       PRELIMINARY;      PRT;      336 AA.
AC   Q92272;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   PUTATIVE POTASSIUM CHANNEL TWIK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA   Kaczmarek L.K.;
RT   "Cloning and localization of rTWIK, a putative potassium channel with
RT   two P domains.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF022819; AAD09336.1; -.
DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   INTERPRO; IPR001779; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01333; 2POREKCHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   336 AA;  38228 MW;  5E78031947D75DE6 CRC64;

Query Match     96.6%;  Score 1693;  DB 11;  Length 336;
Best Local Similarity   96.4%;  Pred. No. 2.9e-130;
Matches  324;  Conservative  6;  Mismatches  6;  Indels  0;  Gaps  0;

Qy    1  MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLILYLVFGAVVFSSVELPYEDLLRQELRKLK  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MLQSLAGSSCVRLVERHRSAWCFGFLVLGYLILYLVFGAVVFSSVELPYEDLLRQELRKLK  60

Qy   61  RRFLEEHECLSEQOLEQOFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120
         |||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  RRFLEEHECLSEPOLEQOFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120

Qy  121  GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180

Qy  181  IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240

Qy  241  FRELYKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIIEHDQLS  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db  241  FRELYKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVHIMEHDQLS  300

Qy  301  FSSITDQAAGMKEDQKQNEPFVATQSSSACVDGPANH  336
         |||||:||||:|||:|||||||||:|| ||   ||
Db  301  FSSITEQAAGLKEEQKQNEPFVASQSPPYEDGSANH  336

RESULT  3
ID   O08581       PRELIMINARY;      PRT;      336 AA.
AC   O08581;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   INWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TWIK-1.
GN   KCNK1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=97165959; PubMed=9013852;
RA   Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RA   Lazdunski M.;
RT   "The structure, function and distribution of the mouse TWIK-1 K+
RT   channel.";
RL   FEBS Lett. 402:28-32(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ; TISSUE=LIVER;
RX   MEDLINE=98218573; PubMed=9559671;
RA   Arighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
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RT   "Structure, chromosome localization, and tissue distribution of the
RT   mouse twik K+ channel gene.";
RL   FEBS Lett. 425:310-316(1998).
CC   -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
CC       KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC       EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
CC       EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC       OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC       MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC       CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC       CORTEX.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC       CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC       STABILIZES AFTER DAY 8.
CC   -!- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC       ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
DR   EMBL; AF033017; AAC16973.1; -.
DR   MGD; MGI:1109322; Kcnk1.
DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   INTERPRO; IPR001779; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01333; 2POREKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN      1     20   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   21     41   POTENTIAL.
FT   DOMAIN    104    130   POTENTIAL.
FT   DOMAIN    133    153   PORE-FORMING (POTENTIAL).
FT   TRANSMEM  154    177   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN    178    198   POTENTIAL.
FT   TRANSMEM  212    238   POTENTIAL.
FT   DOMAIN    247    267   PORE-FORMING (POTENTIAL).
FT   TRANSMEM  268    336   POTENTIAL.
FT   MOD_RES    19     19   CYTOPLASMIC (POTENTIAL).
FT   MOD_RES   303    303   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES    95     95   PHOSPHORYLATION (BY CAM-KINASE II)
FT                          (POTENTIAL).
FT   CARBOHYD  303    303   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   95     95
SQ   SEQUENCE  336 AA;  38275 MW;  A996060A18266F14 CRC64;

Query Match            94.6%;  Score 1658;  DB 11;  Length 336;
Best Local Similarity  94.0%;  Pred. No. 2.1e-127;
Matches  316;  Conservative  10;  Mismatches  10;  Indels  0;  Gaps  0;

Qy    1 MLQSLAGSSCVRLVERHRSAWCGFLVLGYLLLVLVFGAVVFSSVELPYEDLLRQELRKLK   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MLQSLAGSSCVRLVERHRSAWCGFLVLGYLLLVLVFGAVVFSSVELPYEDLLRQELRKLK   60

Qy   61 RRFLEEHECLSEQOLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120
        ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 RRFLEEHECLSEPOLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120

Qy  121 GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTALVQRVTVHVTRRPVLYFHIRWGFSKQVVA  180

Qy  181 IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCF ISLSTIGLGDYVPGEGYNQK 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240

Qy  241 FRELYKIGITCYLLLGLITMLVVLETFCELHELKFRKMFYVKKDKDEDQVHIIEHDQLS  300
        |||||||||||||||||||||||:|||||| |||:|||||||||||||:| ||:|||||
Db  241 FRELYKIGITCYLLLGLITMLVVLETFCELHELKFRKMFYVKRDKDEDLVHIMEHDQLS  300

Qy  301 FSSTTDQAAGMKEDQKQNEPFVATQSSACVDGPANH  336
        |||::|| ||:||:|| ||||| ||||:  || :|
Db  301 FSSVTEQVAGLKEEQKQSEPFVASQSPPYEDGSADH  336
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RESULT 4
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ID   002821                    PRELIMINARY;      PRT;    259 AA.
AC   002821;
DT   01-JUL-1997 (TREMBLrel. 04, Created)
DT   01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT   01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE   DOUBLE PORE POTASSIUM CHANNEL RABKCNK1 (FRAGMENT).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Orias M., Velazquez H., Tung F., Desir G.V.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF004695; AAB61602.1; -.
DR   INTERPRO; IPR001622; -.
DR   INTERPRO; IPR001779; -.
DR   PRINTS; PR01096; TWIK1CHANNEL.
DR   PRINTS; PR01333; 2POREKCHANNEL.
FT   NON_TER     259    259
FT   NON_TER       1      1
SQ   SEQUENCE  259 AA;  29311 MW;  5546ABD278E79F3 CRC64;

Query Match            73.7%;  Score 1292.5;  DB 6;  Length 259;
Best Local Similarity  95.7%;  Pred. No. 9.3e-98;
Matches  247;  Conservative  6;  Mismatches  4;  Indels  1;  Gaps  1;

Qy    1 MLQSLAGSSCVRLVEHRHSAWCGFLVLGYLLLVLVFGAVVFSSVELPYEDLLRQELRKLK   60
        ||||||||||||||||:|| |  |:|:|||||||||||||||:||||||||||||||||||
Db    3 MLQSLAGSSCVRLVERH-TAWCFGFLVLGYLLLVLVFGAVVFSSVELPYEDLLRQELRKLK  61

Qy   61 RRFLEEHECLSEQOLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY  120
        |||:|||||||||||||||||||||:|||||| ||||||||||||:|||||||||||||||
Db   62 RRFVEEHECLSEQOLEQFLGRVLEANNYGVSVRSNASGNWNWDFPASALFFASTVLSTTGY  121

Qy  121 GHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVA  180
        ||||||| ||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  122 GHTVPLSDVGKAFCIIYSVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHVRWGFSKQVVA  181

Qy  181 IVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  240
        ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db  182 IVHAVLLGIITVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQK  241

Qy  241 FRELYKIGITCYLLLGLI  258
        ||||||||||||||||||
Db  242 FRELYKIGITCYLLLGLI  259
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RESULT 5
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ID   Q9Y257                    PRELIMINARY;      PRT;    313 AA.
AC   Q9Y257;
DT   01-NOV-1999 (TREMBLrel. 12, Created)
DT   01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT   01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE   POTASSIUM CHANNEL (TWIK-ORIGINATED SIMILARITY SEQUENCE TOSS).
GN   KCNK6 OR TWIK2 OR TOSS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RX   MEDLINE=99285568; PubMed=10359073;
RA   Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes D.,
```

RA   Saganich M., Rudy B., Artman M., Coetzee W.A.;
RT   "Identification and cloning of TWIK-originated similarity sequence
RT   (TOSS): a novel human 2-pore K+ channel principal subunit.";
RL   FEBS Lett. 450:191-196(1999).
RN   [2]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-53.
RC   TISSUE=BRAIN;
RX   MEDLINE=99175162; PubMed=10075682;
RA   Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
RA   Mehta Y., Forsayeth J.R., Yost C.S.;
RT   "TWIK-2, a new weak inward rectifying member of the tandem pore domain
RT   potassium channel family.";
RL   J. Biol. Chem. 274:7887-7892(1999).
RN   [3]
RP   ERRATUM.
RA   Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
RA   Mehta Y., Forsayeth J.R., Yost C.S.;
RL   J. Biol. Chem. 274:24440-24440(1999).
CC   -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
CC   TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
CC   PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
CC   IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
CC   LOWEST EXPRESSION DETECTED IN BRAIN.
CC   -!- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL
CC   DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC   CHANNELS.
DR   EMBL; AF134149; AAD22980.1; -.
DR   EMBL; AF117708; AAD24000.1; -.
DR   MIM; 603939; -.
DR   INTERPRO; IPR001622; -.
DR   INTERPRO; IPR001779; -.
DR   PRINTS; PR01096; TWIK1CHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Glycoprotein;
KW   Potassium transport; Phosphorylation.
FT   DOMAIN   1   4   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   5   25   POTENTIAL.
FT   DOMAIN   26   89   POTENTIAL.
FT   TRANSMEM   90   115   POTENTIAL.
FT   DOMAIN   115   121   POTENTIAL.
FT   TRANSMEM   121   141   POTENTIAL.
FT   DOMAIN   142   172   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   173   193   POTENTIAL.
FT   DOMAIN   199   223   PORE-FORMING (POTENTIAL).
FT   TRANSMEM   236   256   POTENTIAL.
FT   DOMAIN   257   313   CYTOPLASMIC (POTENTIAL).
FT   MOD_RES   158   158   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES   304   304   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   CARBOHYD   79   79   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   85   85   N-LINKED (GLCNAC...) (POTENTIAL).
FT   MUTAGEN   53   53   C->A: NO CHANNEL ACTIVITY.
SQ   SEQUENCE   313 AA; 33747 MW; 1379382DFB05750E CRC64;

Query Match   37.3%;
Best Local Similarity   45.3%;   Score 653.5; DB 4; Length 313;
Matches 140; Conservative 58; Mismatches 86; Indels 25; Gaps 7;

Qy   24 GFLVLG----YLILVFGAVVFSSVELPYEDLLRQELRLKRRFELEEHECLSEQOLEQFL 79
            ||| ||:::| |||::|:|||:|:||| ||
Db   4 GALLAGALAAVAAVLVLGALLVARLEGPHEARLEAELETLRAQLLORSPCVAAPALDAFV 63

Qy   80 GRVLEASNYGVSVLSNASGNWN------WDFTSALFFASTVLSTGYGHTVPLSDGGKAFC 134
Db   64 ERVLAAGRLGRVVLANASGSANASDPAWDFASALFFASTLITTVGYGYTPLTDAGKAFS 123

Qy   135 IIYSVGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAY-LLGFVTVS 193
Db   124 IAFALLGVPTTMLLLTASAQRLSLLITHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTV 183

Qy   194 CFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYPGEGYNQKFRELYKIGITCYL 253
Db   184 C-FLVPAVIFAHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYL 242

Qy   254 LLGLIAMLLVVLEFCELHELKKFRKMFYV---------KKDKDEDQVHII------EHDQLS 300
Db   243 FLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADED-DRVDLIGPQPESHQQLS 301

Qy   301 FSSITDQAA 309
Db   302 ASSHTDYAS 310

RESULT 6
Q9JJ14
ID   Q9JJ14   PRELIMINARY;   PRT;   343 AA.
AC   Q9JJ14;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TWO PORE DOMAIN K+ CHANNEL SUBUNIT.
GN   KCNK6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/OLA;
RA   Saridaki A., Ferraz C., Demaille J., Scherer G., Roux A.-F.;
RT   "Genomic sequencing reveals the structure of the Kcnk6 and Map3k11
RT   genes and their close vicinity to the Sipa1 gene on mouse chromosome
RT   19.";
RL   Cytogenet. Cell Genet. 89:85-88(2000).
EMBL; AF155142; AAF73282.1; -.
KW   Ionic channel.
SQ   SEQUENCE   343 AA; 35993 MW; 7D3672F3AA284168 CRC64;

Query Match   30.4%;
Best Local Similarity   38.3%;   Score 532.5; DB 11; Length 343;
Matches 124; Conservative 59; Mismatches 124; Indels 17; Gaps 6;

Qy   26 LVLGYLLYLIVFGAVVFSSVELPYEDLLRQELRLKRRFELEEHE-CLSEQOLEQFLGRVLE 84
Db   13 LLMAHLLAMGLGAVVLQALEGPPARHLQAQVQAELASPQAEHRACLPPEALEELLGAVLR 72

Qy   85 ASNYGVSVLSNASGNWNWDFTSALFFASTVLSTGYGHTVPLSDGGKAFCIIYSVGIPF 144
Db   73 AQAHGVSSLGNSSETSNWDLPSALLFIRASILITTGYGHMAPLSSGGRAFCVVYAAGLPA 132

Qy   145 TLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFIPAAVFS 204
Db   133 SLA-LVAALRHCLLPVFSRPGDWVAIRWQLAPAQAALLQAAGLGLLVACVFMLLPALVLW 191

Qy   205 VLEDDWNFLESFYFCFISLSTIGLGDYVP--GEGYNQKFRELYKIGITCYLLLGLIAMLV 262
Db   192 GVQGDCSLLEAIYFCFGSLSTIGLGDILPAHGRGLIHPAIYHLGQFALLGYLLLGLLAML 251

Qy   263 VLETFCELHELKKFRKMFYVKKDK-DEDQVHIIEHDQLSFSSITDQA----------AGMKE 313
Db   252 AVETFSELPQVRAMVKFFGPSGSRTDEDODGILGODELALSTVLPDAPVLGPTTPASVSE 311

Qy   314 DOKONEPPVATOSSAC-----VDGP 333
Db   312 HQNRPQPADPSQATGSQOLDRVGGP 335

RESULT 7
Q9Y2U2
ID   Q9Y2U2   PRELIMINARY;   PRT;   307 AA.
AC   Q9Y2U2; Q9Y2U4; Q9Y2U3;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)

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DE   TWO PORE DOMAIN POTASSIUM CHANNEL PROTEIN KCNK7.
GN   KCNK7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99223496; PubMed=10206991;
RA   Salinas M., Reyes R., Lesage F., Fosset M., Heurteaux C., Romey G.,
RA   Lazdunski M.;
RT   "Cloning of a new mouse two-P domain channel subunit and a human
RT   homologue with a unique pore structure.";
RL   J. Biol. Chem. 274:11751-11760(1999).
CC   -!- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBUNIT. NO CHANNEL ACTIVITY
CC       OBSERVED IN VITRO AS POTASSIUM CHANNEL REMAINS IN THE ENDOPLASMIC RETICULUM.
CC       MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO
CC       REACH THE PLASMA MEMBRANE.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; ISOFORM KCNK7-A (SHOWN HERE),
CC       ISOFORM KCNK7-B AND ISOFORM KCNK7-C; ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
DR   EMBL; AF110522; AAD29578.1; -.
DR   EMBL; AF110524; AAD29580.1; -.
DR   EMBL; AF110523; AAD29579.1; -.
DR   MIM; 603940; -.
DR   InterPro; IPR001622; -.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Alternative splicing.
FT   DOMAIN        1     10    CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     11     31    POTENTIAL.
FT   DOMAIN       92    119    PORE-FORMING (POTENTIAL).
FT   TRANSMEM    120    140    POTENTIAL.
FT   DOMAIN      141    170    CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    171    191    POTENTIAL.
FT   DOMAIN      199    227    PORE-FORMING (POTENTIAL).
FT   TRANSMEM    233    253    POTENTIAL.
FT   DOMAIN      254    307    CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     83     83    N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC    241    252    YLLIGLLAMLLA -> GGTSLQGTAWEG (IN ISOFORM
FT                             KCNK7-B).
FT   VARSPLIC    253    307    MISSING (IN ISOFORM KCNK7-B).
FT   VARSPLIC    241    257    YLLIGLLAMLLAVETFS -> KSSHLTACGGRGKRSLD
FT                             (IN ISOFORM KCNK7-C).
FT   VARSPLIC    258    307    MISSING (IN ISOFORM KCNK7-C).
SQ   SEQUENCE    307 AA;  31946 MW;  BD4A36DD9591ADAC CRC64;

Query Match      29.7%;  Score 521.5;  DB 4;  Length 307;
Best Local Similarity  41.4%;  Pred. No. 7.5e-35;
Matches 120;  Conservative  47;  Mismatches 118;  Indels 5;  Gaps 4;

Qy    23 FGFLVLGYILYLVFGAVVFSSVELPYEDLLRQELRLKRRFLEEHE-CLSEQQLEQFLGR 81
         :|| ::|| :||| |||||| ::||:||                   || :||:|:|
Db    10 YGLLVVAHILALGLGAVVFQALEGPPACRLQAELRAELAAFQAEHRACLPPGALEELGT 69

Qy    82 VLEASNVGVSVLSNASGNWNWDFTSALFFASTVLSTGYGHTVPLSDGGKAFCIIYSVIG 141
         .|:: |:|| |:::| |||||||::::| |||||| ||:||:|||||||| : |::||
Db    70 ALATQAHGVSTLGNSSEGRTWDLPSALLFAASIITTTGYGHMAPLSPGGKAFCMVYAALG 129

Qy   142 IPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGEVTVSCFFIPAA 201
         :|::| |::| :||:|  |:||  : |: |   : :|| |:| |    :||    ::||
Db   130 LPASLA-LVATLRHCLLPVLSRPRAWVAVHWQLSPARAALLQAVALGLIVASSFVLLPAL 188

Qy   202 VFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEG--YNQKFRELYKLGITCYLLIGLLA 259
         | | : || ||.|| |  | || ||| | : :|   :|| |||:||||| ||||||||
Db   189 VLWGLQGDCSLLGAVYFCFSSLSLTIGLEDLLPGRGRSLHPVIYHLGQLALLGYILLGLLA 248

Qy   260 MLVVLETFCELHELKKFRKRKMFYVKKD-KDEDQVHIIEHDQLSFSSITDQA 308
         ||  |||| ||   : ::   |:                   |:
Db   249 MLLAVETFSELPQVRAMGKFRPSGPVTAEDQGGILGQDELALSTLPPAA 298
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RESULT 8
Q9Z2T1

ID   Q9Z2T1      PRELIMINARY;      PRT;   307 AA.
AC   Q9Z2T1; Q9R2A2; Q9R1V1; Q9QYE8; Q9QXY0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TWO PORE DOMAIN POTASSIUM CHANNEL PROTEIN KCNK8 (PUTATIVE POTASSIUM
DE   CHANNEL DD3) (DOUBLE-PORE K CHANNEL 3) (NEUROMUSCULAR TWO P DOMAIN
DE   POTASSIUM CHANNEL).
GN   KCNK8 OR KCNK6 OR KCH3 OR KNOT1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN, AND LUNG;
RX   MEDLINE=99223496; PubMed=10206991;
RA   Salinas M., Reyes R., Lesage F., Fosset M., Heurteaux C., Romey G.,
RA   Lazdunski M.;
RT   "Cloning of a new mouse two-P domain channel subunit and a human
RT   homologue with a unique pore structure.";
RL   J. Biol. Chem. 274:11751-11760(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ishibashi K., Suzuki M., Imai M.;
RT   "Cloning of a new double-pore K channel expressed predominantly in
RT   testis.";
RL   Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 1-289 FROM N.A.
RA   Bockenhauer D., Nimmakayalu M.A., Ward D.C., Goldstein S.A.N.,
RA   Gallagher P.G.;
RT   "Cloning, localization, and expression of the murine 2 P domain
RT   potassium channel KCNK6.";
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 2-307 FROM N.A.
RA   Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA   Kaczmarek L.K.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 15-307 FROM N.A.
RC   TISSUE=BRAIN;
RA   Lopes C.M.B., Buck M., Goldstein S.A.N.;
RT   "A new two P domain potassium channel subfamily from mouse excitable
RT   tissues.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBUNIT. NO CHANNEL ACTIVITY
CC       OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM.
CC       MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO
CC       REACH THE PLASMA MEMBRANE.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: DETECTED IN EMBRYO, EYE, LUNG AND LIVER.
CC       WEAKLY EXPRESSED IN COLON, TESTIS, ATRIA, KIDNEY, INTESTINE,
CC       BLADDER, UTERUS, OVARY, SALIVARY GLAND, THYMUS AND BRAIN. NOT
CC       DETECTED IN BRAIN, CEREBELLUM, SPINAL CORD, HEART, VENTRICLE,
CC       SKELETAL MUSCLE, LIVER, PLACENTA AND PANCREAS. IN THE EYE, HIGHLY
CC       EXPRESSED IN THE RETINAL GANGLION CELL LAYER AND INNER NUCLEAR
CC       LAYER.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
DR   EMBL; AF110521; AAD29577.1; ALT_TERM.
DR   EMBL; AB015729; BAA35074.1; -.
DR   EMBL; AF022820; AAD09337.1; -.
DR   EMBL; AF012820; AAF11603.1; -.
DR   EMBL; AF012344; AAF14528.1; -.
DR   EMBL; AF158234; AAF14528.1; -.
MGD; MGI:1341841; Kcnk8.
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DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01333; 2PORKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN         1     10   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      11     31   POTENTIAL.
FT   DOMAIN                    POTENTIAL.
FT   TRANSMEM      92    118   POTENTIAL.
FT   DOMAIN                    POTENTIAL.
FT   TRANSMEM     120    140   POTENTIAL.
FT   DOMAIN      141    172   PORE-FORMING (POTENTIAL).
FT   DOMAIN                    CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     173    193   POTENTIAL.
FT   DOMAIN                    POTENTIAL.
FT   DOMAIN      199    227   PORE-FORMING (POTENTIAL).
FT   TRANSMEM     233    253   POTENTIAL.
FT   DOMAIN      254    307   CYTOPLASMIC (POTENTIAL).
FT   MOD_RES        3      3   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES      255    255   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES      274    274   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES      276    276   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   CARBOHYD      83     83   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT       1      1   MGS -> TR (IN REF. 4).
FT   CONFLICT       2      2   GS -> TR (IN REF. 4).
FT   CONFLICT       2      3   GS -> THSREFGPGQEGTR (IN REF. 2).
FT   CONFLICT      84     84   G -> S (IN REF. 2, 3, 4 AND 5).
FT   CONFLICT     231    231   YH -> SP (IN REF. 2).
FT   CONFLICT     232    232   T -> P (IN REF. 2).
FT   CONFLICT     293    293
SQ   SEQUENCE   307 AA;  32168 MW;  567D32AE35BA44F CRC64;

Query Match             29.6%;
Best Local Similarity   40.4%;
Matches  116;  Conservative   52;  Mismatches  114;  Indels    5;  Gaps    4;
Score 518.5;  DB 11;  Length 307;
Pred. No. 1.3e-34;

Qy     26 LIVLGYLILYLVFGAAVFSSVELPYEDLLRQELRKLKRRFLEEHE-CLSEQQLEQFLGRVLE  84
          ||: ||| || |||||||
Db     13 LLMAHLLAMGLGAVVLQALEGPPARHLQAQVQAELASFQAEHRACLPPEALEELIGAVLR  72

Qy     85 ASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGPF  144
          : ||| || ||
Db     73 AQAHGVSSLGNGSETSNWDLPSALLFTASILTTTGYGHMAPLSSGGRAFCVVYAALGLPA  132

Qy    145 TLLFLTAVVQRITVHVTVRRPVLYFHIRWGFESKQVVAIVHAVLLGFVTVSCFFIPAAVFS  204
          :|| :
Db    133 SLA-LVAALRHCLLPVFSRPGDWVAIRWQLAPAQAALLQAAGLLVACVFMLLPALVLVLW  191

Qy    205 VLEDDWNFLESFYFCFISLSLSTIGLGDVVP--GEGYNQKFRELYKIGITCYLLIGLIAMLV  262
          ||| :| ||||||| :| |||||||||| | : ||||||||||||||||||: ||||:|||:
Db    192 GVQGDCSLLEAIYFCFGSLSTIGLGDLLPAHGRGLLPAIYHLGQFALLGYLILGLLAMLL  251

Qy    263 VLETFCELHELKFRKMFYVKKDK-DEDQVHIIEHDQLSFSSITDQA  308
          :||| | || ||:|| |:  |   |||| |: || :| :|: |: |
Db    252 AVETFSELPQVRAMVKFFGPSGSRTDEDQDGILGQDELALSTVLPDA  298
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RESULT  9
Q9NEV3

ID   Q9NEV3      PRELIMINARY;      PRT;   392 AA.
AC   Q9NEV3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   Y39B6B.F PROTEIN.
GN   Y39B6B.F.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sulston J.E.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; AL132896; CAB60911.1; -.
SQ   SEQUENCE   392 AA;  45061 MW;  A14CB4FBD02E0D33 CRC64;

Query Match             24.6%;
Best Local Similarity   38.3%;
Matches  101;  Conservative   47;  Mismatches   83;  Indels   33;  Gaps    7;
Score 430.5;  DB 5;  Length 392;
Pred. No. 2.6e-27;

Qy     41 FSSVELPYEDLLRQELRKLKRRFLEE--HECLSEQQLEQFLGRVLEASNYGVSVLSNASG  98
          ||| || :::|| : : |||||| :| |:  |:||||||||||| :::
Db    118 FSRIEYPLEKIEREAYLDYQNWRDRLIQLDIDESEIDKLFLNIREALNGIWMDRNLTS  177

Qy     99 NWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTAVVQRITV  158
          :|| ||| |||| ||:|||||||| :| | :|| |||: |:|||| |||: |:
Db    178 DPNWTFGQAFFFAGTLISTVGYGRVSPRIEYGKLFTILCVIGIPLTIALLSAIVARM--  235

Qy    159 HVTRRPVLYFHIRWGFESKQ------------VVAIVHAVLLGFVTVSCFFIPAAVFS  204
          |:: : ||||: ||: |||: :| : | | :||: | :| :||||||
Db    236 ---REP---SHKLRGLLNQRLGHLFTVNHIQLIHVGVVFASLLFV----FAIPAWVFS  284

Qy    205 VLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLIGLIAMLVVL  264
          :|| ||:|| :|| ||:||:|||||| | |:  |: || |||||| ::| :||: :|| |
Db    285 SIETDWSYLDAFYYCFVSLTTIGLGDFEPGEDDPNQSFRGLYKIGATVILMGGLCCMMLFL  344

Qy    265 ETFCELHELKFR-KMFYVKKDKD  287
          :|| ||| | :|  :| ||:|:|
Db    345 AT--LYDIPQFNLTSFFVKSDEE  365
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RESULT  10
Q9JIS4

ID   Q9JIS4      PRELIMINARY;      PRT;   538 AA.
AC   Q9JIS4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   POTASSIUM CHANNEL TREK-2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Bang H., Kim Y., Kim D.;
RT   "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT   family.";
RL   J. Biol. Chem. 275:17412-17419(2000).
DR   EMBL; AF196965; AAF75132.1; -.
SQ   SEQUENCE   538 AA;  59800 MW;  1FF33F0AA52897E4 CRC64;

Query Match             22.6%;
Best Local Similarity   32.9%;
Matches   94;  Conservative   54;  Mismatches  104;  Indels   34;  Gaps    9;
Score 396;  DB 11;  Length 538;
Pred. No. 2.5e-24;

Qy     25 FIVLGYLILYLVFGAAVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE  84
          |:|| | ::| ||| ||   ||:|  :|:
Db     76 FVVV--VVYLVTGLVFRALEQPFESSQKNTIALEKAEFLRDHCVSPOELEFLIQHALD  133

Qy     85 ASNYGVSVLSNAS-GNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP  143
          | |:|||:  ::: |:  ::||:|:||| |||:| |||::::||: ||:||||||:|::| |
Db    134 ADNAGVSPVGNSSNSSSHWDLGSAFFRAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP  193

Qy    144 FTLLFLTAV------------VQRITVHVTVRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV  192
          : | || |            |||:||| ||||||||||||||| :|
Db    194 LFGFLLAGTGDQLGTIFGKSIARVEKVFRKKQV--------SQTKRVISTLL--FILA  242

Qy    193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYPGEGYNQKFRELYKIGIT  250
          ||       |||:||:|  ||  || :| |||||||||||  |||:|| ||||||||||:
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RESULT 11

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Db  243  GCIVFVTIPAVIFKYIE-GWTALESIYFVVVLLJTVGFGDFVAGGNAGINYREWYKPLVW  301
Qy  251  CVILLGLIAMLVVLETFCE-LHELKKFPRKMFYVKKDKDEDQVHIE                295
Dd  302  FWILVGLAYFAAVLSMIGDWLRVLSK-----KIKEEVGEIKAHAAE                342
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ID   O95069      PRELIMINARY;   PRT;   426 AA.
AC   O95069; Q9UNE3;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   OUTWARD RECTIFYING POTASSIUM CHANNEL TREK-1 (TWO-PORE
DE   POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUEUNIT).
GN   KCNK2 OR TREK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC       CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
DR   EMBL; AF129399; AAD47569.1; -.
DR   EMBL; AF004711; AAD01203.1; -.
DR   MIM; 603219; -.
DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01333; 2PORECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN      1     61    CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    62    82    POTENTIAL.
FT   DOMAIN     144    170   PORE-FORMING (BY SIMILARITY).
FT   TRANSMEM   172    192   POTENTIAL.
FT   DOMAIN     193    223   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   224    244   POTENTIAL.
FT   DOMAIN     253    283   PORE-FORMING (BY SIMILARITY).
FT   TRANSMEM   288    308   POTENTIAL.
FT   DOMAIN     309    426   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN     378    426   ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT                           SENSITIVITY (BY SIMILARITY).
FT   DOMAIN     354    426   REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
FT                           SIMILARITY).
FT   MOD_RES     38     38   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES    315    315   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES    318    318   PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES    343    343   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES    348    348   PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES    360    360   PHOSPHORYLATION (BY PKA) (POTENTIAL).
FT   MOD_RES    366    366   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES    110    110   PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   CARBOHYD   134    134   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CONFLICT     2     16   MISSING (IN REF. 2).
FT   CONFLICT   309    311   RLV -> DWL (IN REF. 2).
FT   CONFLICT   391    391   S -> N (IN REF. 2).
FT   CONFLICT   411    411   A -> T (IN REF. 2).
SQ   SEQUENCE   426 AA;  47016 MW;  2ABA23360009F4E CRC64;
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Query Match             21.8%;  Score 381.5;  DB 4;  Length 426;
Best Local Similarity   32.7%;  Pred. No. 2.8e-23;
Matches   91;  Conservative 61;  Mismatches 107;  Indels 19;  Gaps 9;

Qy   25  FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRLKIRRFLEEHECLSEQOLEQFLGRVLE   84
Db   66  FLVV--VLYLLIGATVFKALEQPHEISQRTTIVIQKOTFISQHSCVNSTELDELIQOIVA  123

Qy   85  ASNYGVSVLSNASGN--WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP  143
Db  124  AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP  183

Qy  144  FTLLFLTAVVQORITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFT--P  199
Db  184  LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP  241

Qy  200  AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA  259
Db  242  AIIFKHIE-GWSALDAIYFVVITLITTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY  299

Qy  260  MLVVLETFCELHEL--KKFRKMFYVKKDKDEDQVHIIE                         295
Db  300  FAAVLSMIGRLVRVISKK-----TKEEVGEFRAHAAE                          331
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RESULT 12

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ID   O88454      PRELIMINARY;   PRT;   398 AA.
AC   O88454;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TWIK-RELATED ARACHIDONIC ACID-STIMULATED POTASSIUM CHANNEL PROTEIN
DE   TRAAK.
GN   KCNK4 OR TRAAK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=98292450; PubMed=9628867;
RA   Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA   Lazdunski M.;
RT   "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT   polyunsaturated fatty acids.";
RL   EMBO J. 17:3297-3308(1998).
RN   [2]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC       EXTERNAL K+ CONCENTRATIONS.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ISOFORM TRAAK (SHOWN HERE)
CC       AND ISOFORM TRAAKT ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC       DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC       TESTIS.
CC   -!- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC       FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC       CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
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Left column

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CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
DR   EMBL; AF056492; AAC40181.1; -.
DR   MGD; MGI:1299234; Kcnk4.
DR   INTERPRO; IPR000099; -.
DR   INTERPRO; IPR001622; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01333; 2POREKCHANNEL.
DR   PRINTS; PR01334; TWIK_channel.
KW   Ionic channel.; Transport; Potassium transport;
KW   Glycoprotein; Alternative splicing; Phosphorylation.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       89    113       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    119    139       POTENTIAL.
FT   DOMAIN      140    171       POTENTIAL.
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      198    222       PORE-FORMING (POTENTIAL).
FT   DOMAIN      235    255       TRANSMEM
FT   DOMAIN      256    398       CYTOPLASMIC (POTENTIAL).
FT   MOD_RES     146    146       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES     262    262       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES     265    265       PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES     284    284       PHOSPHORYLATION (BY CK2) (POTENTIAL).
FT   MOD_RES     288    288       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES     340    340       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES     358    358       PHOSPHORYLATION (BY CAM-KINASE II)
FT                                (POTENTIAL).
FT   MOD_RES     360    360       PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES     379    379       PHOSPHORYLATION (BY CK II) (POTENTIAL).
FT   MOD_RES     383    383       PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   CARBOHYD     81     81       N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC...) (POTENTIAL).
FT   VARSPLIC     63     67       KLIVE -> KAMAI (IN ISOFORM TRAAKT).
FT   VARSPLIC     68     398      MISSING (IN ISOFORM TRAAKT).
SQ   SEQUENCE   398 AA;  43051 MW;  478A834B7B7AEC92 CRC64;

Query Match             21.6%;  Score 379.5;  DB 11;  Length 398;
Best Local Similarity   34.4%;  Pred. No. 3.8e-23;
Matches   90;  Conservative   54;  Mismatches   95;  Indels  23;  Gaps  9;

Qy    18 RSAWCGFIVLGYILYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77
          :| |||| :| | ::| | ||||||:|| :|| |:| ::| | |||| |:| |||||:|
Db     2 RSTTLLALIAL-VLLYLVSGALVFQALEQPHEQQAQREGEVREKFLIRAHPCVSDQELEQ 60

Qy    78 FLGRVLEASNYGVSVLSNASGNWN------------WDFTSALFFASTVLSTTGYGHTVPLSDG 129
          :| :| |::| |:||:|||:|              | : : ||:|||||:| |||| |:|
Db    61 FIKLIVEALGGG---ANPETSWTNSSNHSSAWNLGSAFFSGTIITTIGYGNIVLHTDA 116

Qy   130 GKAFCIIYSVIGIPFTLLFLFTAVVQRITVHVTRRPVLIYFH----IRWGFSKQVVAIVHAVL 186
          |:|||:| || |:||| |::|||:||  : |:|    | |:        | |||||:|||||
Db   117 GRLFCIFYALVGIPLFGMLLAGVGDRLGSSL-RRGIGHIEAIFLKWHVPPGLVRSLSAVL 175

Qy   187 LGEVTVSCFFFI---PAAVFSVLEDDWNFLESFYCFISLSTIGLGDYVPGEGYNQKFREL 244
          | |:| | |||    ::| |:: |||| : | |  | ||:|||||||||| |||| |||
Db   176 --FLLIGCLLFVLFPTFVFSYME-SWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPA 231

Qy   245 YKIGITCYLLLGLIIAMLVVLET 266
          | | | || |: ||| | || |
Db   232 YQPLVWFWILFGLAYFASVLTT 253
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Right column

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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA   Medhurst A.D., Murdock P., Chapman C.G.;
RT   "Cloning, localization and functional expression of the human ortholog
RT   of the TREK-1 potassium channel.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF171068; AAF89743.1; -.
KW   Ionic channel.
SQ   SEQUENCE   411 AA;  45494 MW;  FDE40CAB21B42A1C CRC64;

Query Match             21.6%;  Score 379.5;  DB 4;  Length 411;
Best Local Similarity   32.5%;  Pred. No. 4e-23;
Matches   90;  Conservative   62;  Mismatches  108;  Indels  17;  Gaps  9;

Qy    25 FLVLGLYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84
          ||:   |:|| |: | | ::| | |||::| |:| : | || |:| ||||||||:|:| |
Db    51 FLVV--VLYLIGATVFRALEQPHEISQRTTIVIQKQFISQHSCVNSTELDELIQOIVA 108

Qy    85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143
          | |  |:|| ||| | | |: : :|||||||:| |||||||| |:|| |||:| || |
Db   109 AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGRKFICIIYALGIP 168

Qy   144 FTLLFLTAVVQRITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI--P 199
          ||| |:||:||  | |:    | |  |  | | ||||:|:|||:|||| ||:|||:   |
Db   169 LFGFLLAGVGDQLGTIFGKGIARKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP 226

Qy   200 AAVFSVLEDDWNFLESFYCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA 259
          ||||: |||||: | ||  | ||:|||||||| ||||:|::| | ||: | || |:
Db   227 AIIFKHIE-GWSALDAIFVVILTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY 284

Qy   260 MLVVLEFPCE-LHELKFPRKMFYVKDKDEDQVHIIE 295
          :|  |:     | | || :| : : | |:
Db   285 FAAVLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 316
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RESULT  14
ID   Q9NYG8     PRELIMINARY;   PRT;   419 AA.
AC   Q9NYG8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   TANDEM PORE DOMAIN POTASSIUM CHANNEL TRAAK.
GN   KCNK4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=FRONTAL LOBE;
RA   Gray A.T.;
RT   "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT   chromosome 11.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF247042; AAF64062.1; -.
KW   Ionic channel.
SQ   SEQUENCE   419 AA;  45189 MW;  E7C8E57A35C4FBF CRC64;

Query Match             21.6%;  Score 378;  DB 4;  Length 419;
Best Local Similarity   33.7%;  Pred. No. 5.4e-23;
Matches   88;  Conservative   53;  Mismatches   98;  Indels  22;  Gaps  8;

Qy    18 RSAWCGFIVLGYILYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQ 77
          :| |||| :|  | ::| | ||||||:|| :|| |:| ::| | |||| |:| ||||||:
Db    28 RSTTLLALIAL-VLLYLVSGALVFRALEQPHEQQAQRELEGEVREKFLIRAHPCVSDQELGL 86
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Qy    78 FLGRVLEASNYGVSVLSNASGNWN---WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFC 134
            |:|   ||  ||:|::|| :|:||||||| : ||  ||
Db    87 LIKEVADALGGGADPEPNSTSNSSHSAWDLGSAFFFSGTITIIIGYGNVALRTDAGRLFC 146

Qy   135 IIYSVIGIPFTLLFLTAVVQRI-----------THVHTRRPVLYFHIRWGFSKQVVAIVHAVLL 187
            |::|||     |:| : ||:|  ||  |
Db   147 IFYALVGIPLFGILLAGVGDRLGSSLRHGIGHIEA-----IFLKWHVPPELVRVLSAML- 200

Qy   188 GFVTVSCFFFI--PAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELY 245
            :|: :|| |   ||||| |:||:||:||||| ||:|||||||||| |||:||||:||||
Db   201 -FLLIGCLLFVLPTFVPCYME-DWSKLEAIYFVIVTLTTVGFGDYVAGADPROD-SPAY 257

Qy   246 KIGITCYLLLGLIAMLVVLET 266
            ||| ||:|||:|||:|||||
Db   258 QPLVWFWILLGLAYFASVITT 278
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RESULT 15
P97438

ID   P97438   PRELIMINARY;   PRT;   411 AA.
AC   P97438;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-1 (TWO-PORE
DE   POTASSIUM CHANNEL TPKC1) (TREK-1 K+ CHANNEL SUBUNIT).
GN   KCNK2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=BRAIN;
RX   MEDLINE=97157476; PubMed=9003761;
RA   Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RT   "Cloning, functional expression and brain localization of a novel
RT   unconventional outward rectifier K+ channel.";
RL   EMBO J. 15:6854-6862(1996).
RN   [2]
RP   REVISIONS.
RC   TISSUE=BRAIN;
RA   Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC   DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC   LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC   HIPPOCAMPUS AND CEREBELLUM.
CC   -!- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC   ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC   ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC   CHANNELS.
DR   EMBL; U73488; AAC53005.2; -.
DR   MGD; MGI:109366; Kcnk2.
DR   INTERPRO; IPR000009; -.
DR   INTERPRO; IPR001622; -.
DR   PFAM; PF02034; TWIK_channel; 1.
DR   PRINTS; PR01333; 2PORECHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Phosphorylation.
FT   DOMAIN   1   46   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   47   67   POTENTIAL.
FT   DOMAIN   129   155   PORE-FORMING (POTENTIAL).
FT   TRANSMEM   157   177   POTENTIAL.
FT   DOMAIN   178   207   CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   208   228   POTENTIAL.
FT   DOMAIN   238   268   PORE-FORMING (POTENTIAL).
FT   TRANSMEM   273   293   POTENTIAL.
FT   DOMAIN   294   411   CYTOPLASMIC (POTENTIAL).
FT   DOMAIN   354   411   ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT   SENSITIVITY.
FT   DOMAIN   23   23   REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT   MOD_RES   328   328   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES   333   333   PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES   345   345   PHOSPHORYLATION (BY PKC) (POTENTIAL).
FT   MOD_RES   351   351   PHOSPHORYLATION (BY CAPK) (POTENTIAL).
FT   MOD_RES   303   303   PHOSPHORYLATION (BY CAM-KINASE II)
FT   (POTENTIAL).
FT   CARBOHYD   119   95   N-LINKED (GLCNAC...) (POTENTIAL).
FT   CARBOHYD   95   95   N-LINKED (GLCNAC...) (POTENTIAL).
SQ   SEQUENCE   411 AA; 45297 MW; 8F97GDDD103EFA05 CRC64;

Query Match   21.5%;   Score 376.5;   DB 11;   Length 411;
Best Local Similarity   32.5%;   Pred. No. 7e-23;
Matches   90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

Qy   25 FLVLGYLILLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84
            |||:|||||:||||||:||:|||||||:||::||||||||||||:|||||||:||||||
Db   51 FLVV--VLYLLIGAAVFKALEQPQEISQRTTIVIOKQTFIAQHACVNSTELDELIQQIVA 108

Qy   85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143
            | |:| |:||::| :| ||:||||||:||||||:|||||||:|:||||| :||:|||
Db   109 AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP 168

Qy   144 FTLLFLTAVVQRITVHVTR--RPVLFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI--P 199
            | :|| ||:|:|: : | |:|:|:|||| |||||:|||||||||:|||||||: |
Db   169 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP 226

Qy   200 AAVFSVLEDDWNFLESFYFCFISLSLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA 259
            |:|| :|:|||:||:|||||:|:||||:||||||| ||:|:|:||:| ||:|||:|||:
Db   227 AVIFKIHIE-GWSALDAIYFVVITLLTTIGFGDYVAG-GSDIEYLDFYKPVVWRWILVGLAY 284

Qy   260 MLVVLETFCE-LHELKFKRKMFYVKDKDEDQVHIIE 295
            :|:|| || : || :| : |: |:|||:|| |:|
Db   285 FAAVLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 316
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Search completed: February 14, 2001, 03:34:29
Job time: 28101 sec